

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2002, 04:48:40 ; Search time 63 Seconds

(without alignments)
3261.818 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 2802

Sequence: 1 MRSDKSAVFLILQLFCVGC.....KCFLESCQKFNKTRIEKRE 527

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 350425 segs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2797	99.8	3006	9	US-09-962-678-1	Sequence 1, Appl1
6	1721.5	61.4	1889	9	US-09-981-353-83	Sequence 83, Appl1
7	1713	61.1	2090	10	US-09-880-107-3292	Sequence 3292, Ap
8	1691.5	60.4	2130	9	US-09-981-353-45	Sequence 45, Appl1
9	1689	60.3	2093	10	US-09-880-107-3842	Sequence 3842, Ap
10	1685	60.1	1961	10	US-09-917-800A-1403	Sequence 1403, Ap
11	1684	60.1	1713	9	US-09-880-107-3286	Sequence 3286, Ap
12	1676.5	59.8	2124	9	US-09-981-353-193	Sequence 193, Appl
13	1676.5	59.8	1855	10	US-09-880-107-2120	Sequence 2120, Ap
14	1635.5	58.4	2799	10	US-09-880-107-3756	Sequence 3756, Ap
15	1604.5	57.3	1712	9	US-09-981-353-189	Sequence 189, Appl
16	1137	40.6	2349	12	US-09-981-353-151	Sequence 151, Appl
17	1137	40.6	2349	12	US-10-044-090-845	Sequence 845, Appl
18	1093.5	39.0	2320	10	US-09-835-082-1	Sequence 1, Appl1
19	1093.5	39.0	2320	10	US-09-835-082-3	Sequence 3, Appl1
20	1077	38.4	2422	10	US-09-880-107-2106	Sequence 2106, Ap
21	1076.5	38.4	2380	12	US-10-044-090-816	Sequence 816, Appl
22	1076.5	38.4	2385	9	US-09-981-353-153	Sequence 153, Appl
23	821.5	29.3	2448	10	US-09-967-768A-187	Sequence 187, Appl
24	755.5	27.0	735	10	US-09-305-856B-17	Sequence 17, Appl
25	700.5	25.0	2074	10	US-09-822-830A-262	Sequence 262, Appl
26	698.5	24.9	1851	10	US-09-740-029-1	Sequence 1, Appl1
27	697.5	24.9	1572	10	US-09-895-728-3	Sequence 3, Appl1
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31	597	21.3	601	10	US-09-917-800A-1433	Sequence 1433, Ap
32	573	20.4	419	10	US-09-960-352-9640	Sequence 9640, Ap
33	565	20.2	588	10	US-09-833-381-344	Sequence 344, Appl
34	562	20.1	582	10	US-09-867-701-1453	Sequence 1453, Appl
35	557	19.9	378	10	US-09-960-352-13060	Sequence 13060, Ap
36	554	19.8	426	10	US-09-960-352-13860	Sequence 13860, A
37	502	17.9	416	10	US-09-960-352-12236	Sequence 12236, A
38	486	17.3	370	10	US-09-960-352-3236	Sequence 3236, Ap
39	455	16.2	417	10	US-09-960-352-11024	Sequence 11024, A
40	441	15.7	334	9	US-09-981-353-149	Sequence 149, Appl
41	436	15.6	345	10	US-09-960-352-8015	Sequence 8015, Ap
42	409.5	14.6	381	10	US-09-960-352-2070	Sequence 2070, Ap
43	398	14.2	413	10	US-09-960-352-3208	Sequence 3208, Ap
44	391	14.0	391	10	US-09-738-873-21	Sequence 21, Appl
45	386.5	13.8	350	10	US-09-960-352-2069	Sequence 2069, Ap

ALIGNMENTS

RESULT 1
US-09-981-353-165
Sequence 165, Application US/09981353
Patent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981.353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 165
LENGTH: 1636
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO. US20020160382A1 2434655CB1
US-09-981-353-165

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Best Local Similarity: 100.00%
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Mismatch: 0
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D	b	90	GGATTTCTGTGGAAAGCTCGTGTGTGACCTGTGCATGAGCCATTGCTTAATGTCAAG	149
O	y	41	ValIleuGluGluLeuIleValArgGlyHisGluValThrValLeuThrHisSerLys	60
D	b	150	GTCATTCAGAAAGGCTCAATAGTAGAGGCGCAAGAGTAAGTATGTACTCACTCAAG	209
O	y	61	ProSerLeuIleAspTrrArgLysProSerAlaLeuLysPheGluValValHisMetPro	80
D	b	210	CCTTCGTTAATATGACTACAGAAAGCCTTCCTGCATTAAATTTGAGGTGCTCATTTGCCA	269
O	y	81	GlnAspArgThrGluGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly	100
D	b	270	CAGACAGACAGACAGAAATGAAATATTTGTTGACCTGCTGTGAATGCTTGGCAGGC	329
O	y	101	LeuSerThrTrrPglInservalIleLysLeuAsnAspPhePheValGluIleArgGlyThr	120
D	b	330	TTATTCACCTGGCGAATAGTTATTAATAATTAAGATTTTTTTTGTTCAAATAAGAGAACT	389
O	y	121	LeuLysMetCysGluSerPheIleTyrAsnGluThrLeuMetLysLysLeuGlnGlu	140
D	b	390	TTAAAAATGATGTGTGAGACTTTATCTCAATACACACCTTATGAGAAAGCTTACAGAA	449
O	y	141	ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu	160
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O	y	161	LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysMetCyluArg	180
D	b	510	TTTGCTTCAGAGCCCTTTTGCTGCACACTTGAATTTCTGTAGAGGCAATGTGAGCGA	569
O	y	181	SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrCyluLeuThr	200
D	b	570	AGCTGTGGAAAGCTTCCAGCTCCACTTTCTATGTACTCTGTGCTTGTACAGAGTTACA	629
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D	b	750	CCCACTACATTATGTGAGCTGTGGGAAAGCTGCAATATGTCTAATACGAACATAATGG	809
O	y	261	AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyLysLeuHisCys	280
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D	b	870	AAACCTCCAAAGCTTTGGCTTAAGAAATGGAATAATTTGTCCAGATTCACAGGAAAGAT	929
O	y	301	GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluGluLysAlaAsn	320
D	b	930	GGTATTTGGGTTCCTCTGGGGTCACTGTTCCTCAAAAGTTTACGAAAGAAAGGCTATAT	989
O	y	321	IleIleIleSerAlaLeuAlaGlnIleProGlnLysValLeuTrrArgTyrLysGlyLys	340
D	b	990	ATCATTCCTTCAGGCCCTTGGCCAGATCCCAAGAAAGTGTATGGAGGTACAAAGAAAA	1049
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Db	1290	GAAGATTTACAGAGGCGCTTGGAGAACAGTCATTACCGATTCCCTTATTAACGAATGCT	1349
Oy	441	MetKrGLeuSerArGIIleHtSHtSAspGInProValLyProLeuAspArgAlaIaIaPhe	460
Db	1330	ATGGAATTATACAAATTCACCATGATCAACCTGTAAAGCCCTTGATGAGACACTTTC	1409
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Patent No. US20020127584A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Chen, Jian			
APPLICANT: Desnoyers, Luc			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Pan, James			
APPLICANT: Smith, Victoria			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Wood, William I.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
FILE REFERENCE: P9430R1C1			
CURRENT APPLICATION NUMBER: US/10/052,586			
CURRENT FILING DATE: 2002-01-15			
PRIOR APPLICATION NUMBER: 60/059263			
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PRIOR FILING DATE: 1997-09-18			
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PRIOR APPLICATION NUMBER: 60/063564			

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Guney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRA
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P343061C1
; CURRENT APPLICATION NUMBER: US/10/05
; CURRENT FILING DATE: 2002-01-15
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Alignment Scores:
Pred. No.: 0 Length: 2974
Score: 2802.00 Matches: 527
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-784-340-2 (1-527) x US-10-052-586-521 (1-2974)

OY 1 MetArgSerAspLysSerAlaLeuValPheLeuLeuLeuGlnLeuPheCysValIglyCys 20
    |||||
DB 27 ATGAGGCTCGACAAAGTCAGCTTTGGTATTCTCTCTGAGCTCTTCGTGGCTG 86
OY 21 GlyPheCysGlyLysValLeuValTrrProCysAspMetSerIstrrPheAsnValLys 40
    |||||
DB 87 GGATTCTGGGAAATCCCTGGGTGGCCCTGGACATGAGCCATTGCTTAATGTCAG 146
OY 41 ValIleLeuGlnGluLeuIleValArgGlyHisGluValThrValLeuThrHisSerLys 60
    |||||
DB 147 GTCATTCTGAAGAGCTCATAGTGAGAGGCCATGAGTAAACATATTGACTCTCAAG 206
OY 61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGluValValHisMetPro 80
    |||||
DB 207 CCTTCGTTAATTGACTACAGGAAGCCCTTCGCAATTGAAATTTGAGCGTGCCTATGCGCA 266
OY 81 GlnAspArgThrGlnGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
    |||||
DB 267 CAGGACAGAAAGAAATAATGAATATTGTTGACCTGACCTGAAATGCTTGGCAGGC 326
OY 101 LeuSerThrTrrPglInsErValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
    |||||
DB 327 TTATCAACCTGGCAATCAGTTATTAATAATGATTTTTTTGTTGAAATTAAGAGAACT 386
OY 121 LeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
    |||||
DB 387 TTAATAAATGATGTGAGAGCTTATCTCAACCAACAGCCTTAATGAAGAAGCTACAGGAA 446
OY 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
    |||||
DB 447 ACCAACTAGAGTATATGCTTATAGACCTGTGATTCCTCTGGAGAACCTGATGGCTGAG 506
OY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGluArg 180
    |||||
DB 507 TTGCTTGCAAGTCCTTTTGCTGCTACACATTAGAAATTTCTGTAGAGAGCAATATGAGCGCA 566
OY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
    |||||
DB 567 AGCTGTGGGAAATCTCCACCTCCACTTCTTAATGCTACCTGTGCTGACAGACTAACA 626
OY 201 AspArgMetThrPheLeuGlnArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
    |||||
DB 627 GACAGAAATGACCTTTCTGGAAAGAGTAAAAAATTCATATGCTTTTCAGTTTGTTCACCTTC 686
OY 221 TrrPleGlnAspTyrAspTyrHisPheTrrPglGluLysPheTyrSerLysAlaLeuGlyArg 240
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DB 687 TGGATTCCAGATTACGACTATCATTTTGGGAAGAGCTTTTATAGTAAGCATTAGGACG 746
OY 241 ProThrThrLeuCysGluThrValGlyLysAlaGluIleTrrPleuIleArgThrTrrP 260
    |||||
DB 747 CCCACTACATTTATGTAGACTGTGGGAAAAAGCTGACATATGCTTAATACGACATATTGG 806
OY 261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyLysLeuHisCys 280
    |||||
DB 807 GATTTTGAATTTCTTCACCAATACCACTTAACCTTTGAGTTGTGTGGAGATTGACCTGT 866
OY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyLysAsp 300
    |||||
DB 867 AAACCTGCCAAAGCTTTGGCTTAAGGAAATGGAATTTTGTCCAGAGTTCCAGGGAGAGT 926
OY 301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluLysAlaAsn 320
    |||||
DB 927 GGTATTGTGGTGTCTCTGGGGTCTACTGTTCAAAAATGTTACAGAAAAAGCGCTAAT 986
OY 321 IleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrrArgTrrLysGlyLys 340
    |||||
DB 987 ATCATTGCTTCAGCCCTTCCAGATCCACAGAGGTGTATGAGGTACAGGAGGAAAAA 1046
OY 341 LysProSerThrLeuGlyLysAlaAsnThrArgLeuTyrAspTrrPleProGlnAsnAspLeu 360
    |||||
DB 1047 AAACCATCCACATTTAGAGCCCAATACTGGCGTGTATGATTGATNCCAGAAATGATCTT 1106
OY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTrrGlu 380
    |||||
DB 1107 CTGGTCATCCCAAAACCAAGCTTTATCACTCAAGTGGAATGAAATGAGATCTATGAA 1166
OY 381 AlaIleTrrHisGlyValProMetValIglyValProIlePheGlyAspGlnLeuAsn 400
    |||||
DB 1167 GCTATTACCATGGGGTCCCTATGTGGAGGTCCCATATTGGTATGAGCTTGATAAC 1226
OY 401 IleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSer 420
    |||||
DB 1227 ATAGCTCACATGAGGCCAAAGAGCAGCTGTAGAAATTAACCTCAAACTATGACAAAGC 1286
OY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTrrLysGluAsnAla 440
    |||||
DB 1287 GAAGATTACTGAGGGCTTTGAGAACAGTCATTCAGATTCCTCTTAATAAGATGCT 1346
OY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
    |||||
DB 1347 ATGAGATTTCAGAAATTTACCATGATCAACCTGTAAAGCCCTTATGATGACAGACTTTC 1406
OY 461 TrrPleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
    |||||
DB 1407 TGGATGAGTTTGTATGGCCACAAAGAGCAGCAGCAGCTGCGATCAGCTGCCATGAC 1466
OY 481 LeuThrTrrPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
    |||||
DB 1467 CTCACCTGTGTCAGACACACTATAGATGTGATGGGTCTCTGTGACCTGTGGCA 1526
OY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
    |||||
DB 1527 ACTGCTAATTTCTTGTTCACAAAATGTTTTTATTTTCTGTCAAAAATTTAATAAATCT 1586
OY 521 ArgLysIleGluLysArgGlu 527
    |||||
DB 1587 AGAAAGATGAAAAAGAGGAA 1607
    |||||

RESULT 4
US-09-962-678-3
; Sequence 3, Application US/09962678
; Patent No. US20020155499A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; TITLE OF INVENTION: 32624, A NOVEL HUMAN UDP-GLUCURONOSYL
; TITLE OF INVENTION: AND UDP-GLYCOSYL TRANSFERASE AND USES THEREOF
; FILE REFERENCE: 10448-094001
; CURRENT APPLICATION NUMBER: US/09/962,678
; CURRENT FILING DATE: 2001-09-25
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; PRIOR APPLICATION NUMBER: 60/235,044
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-678-3

Alignment Scores:
Pred. No.: 0 Length: 1584
Score: 2797.00 Matches: 526
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.82% Indels: 0
Gaps: 0

US-09-784-340-2 (1-527) x US-09-962-678-3 (1-1584)

QY 1 MetArSerAspLysSerAlaLeuValPheLeuLeuLeuGlnLeuPheCysValGlyCys 20
    |||
Db 1 ATGAGGCTGACAGCTAGCTTGGATTCTGCTCTCGAGCTCTCTGTGGCTGT 60
QY 21 GlyPheCysGlyLysValLeuValTrpProCysAspMetSerHisTrpLeuAsnValLys 40
    |||
Db 61 GGATTCTGTGGAAAGCTGTGGTGGCTGTGACATGAGCCATTTGGCTTAATGTCAAG 120
QY 41 ValLeuLeuGlnLeuLeuValLeuValArgGlyHisGlnValThrValLeuThrHisSerLys 60
    |||
Db 121 CTCATTCTAGAGAGCTCATAGTGAAGCCATGAGTAAACATTAATGACTCACTCAAG 180
QY 61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGlnValValHisMetPro 80
    |||
Db 181 CCTTCGTTAATTGACTACAGAGACCTTCTCATTTGAATTTGAGGTCCATATGCCA 240
QY 81 GlnAspArgThrGlnGluAsnGlnIlePheValAspLeuAlaLeuAsnValLeuProGly 100
    |||
Db 241 CAGAGCAGACAGAGAAATGAAATATTTGTGACCTAGCTCGAATGCTTCCAGGC 300
QY 101 LeuSerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
    |||
Db 301 TTATCAACCTGCGCAATCAGTTATTAATTAATGATTTTGTGTAATTAAGGGAAC 360
QY 121 LeuLysMetLysGlnUserPheIleThrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
    |||
Db 361 TTTAAATGAGTGTGAGAGCTTATCTACATCAGAGCGCTTAATGAGAGAACTCAGGAA 420
QY 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
    |||
Db 421 ACCAACTACGATGATATGCTTATAGACCTTGATCCCTGTGGAGACCTGATGCTGAG 480
QY 161 LeuLeuAlaValProPheValLeuThrLeuArgLieserValGlyGlyAsnMetGlnArg 180
    |||
Db 481 TTGCTTGACAGTCCCTTTGTGCTCAGACTTGAATTTCTGAGGAGGCAATAGAGGA 540
QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
    |||
Db 541 AGCTGTGGAAACTTCCAGCTCCACTTCTCTATGACTGTGCTCATATCAGAGCTAAC 600
QY 201 AspArgMetThrPheLeuGlnLysValLysAsnSerMetLeuSerValLeuPheHisPhe 220
    |||
Db 601 GACAGAAATGACCTTCTCGAAAGAGCTAAATAATCAATGCTTTCAGTTTGTTCACATTC 660
QY 221 TrpIleGlnAspTyrAspTyrHisPheTrpGlnGluPheTyrSerLysAlaLeuGlnArg 240
    |||
Db 661 TCGATTTCAGAGATTACAGATCATATTGTTGGGAAGGTTTATAGTAAGCAATTAGGAAG 720
QY 241 ProThrThrLeuLysGlnThrValGlyLysAlaGlnIleTrpLeuIleArgThrTyrTrp 260
    |||
Db 721 CCCACTACATTTATGTGAGCTGTGGAAAGCTGAGATATGCTTAATACGAACATATTTGG 780
QY 261 AspPheGlnPheProGlnProTyrGlnProAsnPheGlnPheValGlyGlyLeuHisCys 280

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Db 781 GATTTTGAAATTTCTCCACACATACACACTTGTGATTGTTGGAGGATTCACATGT 840
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QY 281 LysProAlaLysAlaLeuProLysGlnMetGlnAsnPheValGlnSerSerGlyLysLys 300
    |||
Db 841 AAACCTGCCAAAGCTTTGGCTTAAGGAAATGGAATAATTTTGTCCAGATTCAGGGAAAT 900
QY 301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGlnLysAlaAsn 320
    |||
Db 901 GGATTGTGGTCTTTCTGTGGGTGCTACTGTTTCAAAATGTTACGAAAGCAAGCTTAAT 960
QY 321 IleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrpArgTyrLysGlyLys 340
    |||
Db 961 ATCATGCTTCAGCCCTTCCAGATCCACAGAAAGGTATGAGAGGTACAAAGAAAA 1020
QY 341 LysProSerThrLeuGlnLysAlaSerThrArgLeuTyrAspTrpIleProGlnAsnAspLeu 360
    |||
Db 1021 AAACCATCCACATTAAGAGCCATACCTCGGCTGTATGATGATGATCCCGAATGATCTT 1080
QY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlu 380
    |||
Db 1081 CTGGTCATCCCAAAACCAAGCTTTATCATCTCATGATGATGATGATGATGATGATGAA 1140
QY 381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
    |||
Db 1141 GCTATTACCATGGGGTCCCTATGCTGAGGAGTCCCATATTTGCTGATCAGCTGTGTAAC 1200
QY 401 IleAlaHisMetLysAlaLysGlyAlaValGlnIleAsnPheLysThrMetTrs 420
    |||
Db 1201 ATAGCTCACATGAGGCGCAAGAGAGCAGCTGTGAATTAATCTCAAACTATGACAAAC 1260
QY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
    |||
Db 1261 GAAGATTATTCAGGGGCTTTGAGAACAGTATACCATTCAGATCTCTTAAGAAGATGCT 1320
QY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
    |||
Db 1321 ATGAGATTATCAAGAAATCCACATGATCAACCTGTAAAGCCCTTAATGACAGAGCTTTC 1380
QY 461 TrpIleGlnPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
    |||
Db 1381 TGGATCAGATTGTGATCAGCCGCCCAAGAGCCAGACAGCTGCGATCAGCTGCCATGAC 1440
QY 481 LeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
    |||
Db 1441 CTCACCTGTTCCAGACACTACTATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
    |||
Db 1501 ACTGCTATATTCCTGTCACAAATGTTTATTTTCTCTGCTGCAAAATTTAATAAACT 1560
QY 521 ArgLysIleGlnLysArgGlu 527
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Db 1561 AGAAAGATAGAAAGAGAGGAA 1581

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RESULT 5
US-09-962-678-1
; Sequence 1, Application US/09962678
; Patent No. US20020155499A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; TITLE OF INVENTION: 32624, A NOVEL HUMAN UDP-GLUCURONOSYL
; TITLE OF INVENTION: AND UDP-GLYCOSYL TRANSFERASE AND USES THEREOF
; FILE REFERENCE: 10448-094001
; CURRENT APPLICATION NUMBER: US/09/962,678
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,044
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(1613)
US-09-962-678-1

Alignment Scores:
Pred. No.: 0 Length: 3006
Score: 2797.00 Matches: 526
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.82% Indels: 0
DB: 9 Gaps: 0

US-09-784-340-2 (1-527) x US-09-962-678-1 (1-3006)

QY 1 MetArgSerAspLysSerAlaLeuValPheLeuLeuGlnLeuPheCysValGlyCys 20
DB 33 ATGAGGCTGACACAGCTTGGTATTTCTGCTCCGACACTCTTCTGTGGCTCT 92
QY 21 GlyPheCysGlyLysValLeuValTProCysAspMetSerHisTrieuAsnValLys 40
DB 93 GGATTCCTGGGAAAGTCCTGGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAG 152
QY 41 ValIleLeuGlnGluLeuIleValArgGlyHisGluValThrValLeuThrHisSerLys 60
DB 153 GTCATCTTGAAGAGCTCATAGTGAAGGCCATGAGGTACAGTATTGCACTCAATGAG 212
QY 61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGluValValHisMetPro 80
DB 213 CCTGCTTAATGACATACAGAAAGCCTTCTGCATTGAATTGAGGTGGCTCATATGCCA 272
QY 81 GlnAspArgThrGlnGlnAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
DB 273 CAGGACAGACAGAAAGAAATATTGTTGACCTGACCTGTAATCTTGGCCAGGC 332
QY 101 LeuSerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
DB 333 TTATCAACCTGGCANTCACTTATAAATTAATGATTTTCTTGTGAATTAAGAGAACT 392
QY 121 LeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
DB 393 TTTAAATATGATGTGTGAGAGCTTTATCTACAAATCAGACCTTATGAAGAAGCTACAG 452
QY 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
DB 453 ACCAATCTGACGATGATAGCTTATAGACCTGTGATTCCCTGTGAGACCTGATGGCTGAG 512
QY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGluArg 180
DB 513 TTGCTTGCAGTCCCTTTTGTGCTCACACTTACAAATTTCTGTAGGAGCAATATGGAGCGA 572
QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
DB 573 ACCTGTGGGAAACCTCCACACTTCTCTATGTAACCTGTGCTCATGACAGACTAACA 632
QY 201 AspArgMetThrPheLeuGlnArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
DB 633 GACAAATATGACCTTCTGTGAAAGAGTAAATAATTCATAGTCTTTCAGTTTGTTCACACTTC 692
QY 221 TPPIleGlnAspTyrAspTyrHisPheTrpGluGluPheTyrSerLysAlaLeuGlyArg 240
DB 693 TGGATTCCAGATTACGACATCATTTTGGGAAGATTTTAATAGTAGGCAATTAGGAAAG 752
QY 241 ProThrThrLeuCysGluThrValGlyLysAlaGluIleTrpLeuIleArgThrTyrTrp 260
DB 753 CCCACTACATTAATGTAGAGACTGTGGAAAAGCTGAGATATGCTAATATAGACATATTGG 812
QY 261 AspPheGlnPheProGlnProTyrGlnProAsnPheGluPheValGlyLysLeuHisCys 280
DB 813 GATTTTGAATTTCTCCACCAATACCAACTTAACCTTGAATTTGTGGAGATTGGCACTCT 872
QY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyLysAsp 300
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DB 873 AATCCTGCCAAAGCTTTGGCTTAAGGAAATGAAATTTTGTCCACAGTTCCAGGCAAGAT 932
QY 301 GlyIleValAlaPheSerLeuGlySerLeuPheGlnAsnValThrGluLysAlaAsn 320
DB 933 GGTATTGTGCTTTTCTGTGGGTACACTTTTCAAAATGTTACAGAAAGAAAGCTAAT 992
QY 321 IleIleIleSerAlaLeuAlaGlnIleProGlnLysValLeuTrpArgTyrLysGlyLys 340
DB 993 ATCATTTGCTTCCAGCCCTTCCGACATCCACAGAAAGCTGTATGGAGGTACAAAGGAAA 1052
QY 341 LysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrpIleProGlnAsnAspLeu 360
DB 1053 AATCCATCCACATTTAGAGCCAAATCTCGGCTGTATGATGGATACCCACGAATATCTT 1112
QY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlu 380
DB 1113 CTGGCATCCCAAAACCAAGCTTTTATCACTCATGGTGAATGAATGGATCTATGAA 1172
QY 381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
DB 1173 GCTATTACCATGGGGTCCCTATGGTGGAGATTCCCATATTTGGTATCAGCTTATAC 1232
QY 401 IleAlaHisMetLysAlaLysGlyAlaAlaValAlaGluIleAsnPheLysThrMetThrSer 420
DB 1233 ATAGCTCAGATGAAGGCCAAAGAGCAGCTGTAGAAATTAATTAACAAACTTGAACAG 1292
QY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
DB 1293 GAAGATTATTCAGAGGCTTTGAGAAGAGTCATTACCGATTCTCTTATTAAGAAATGCT 1352
QY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
DB 1353 ATGAGATTATCAAGAAATTCACATGATCAACCTGTAAACCCCTGTGATCAGACGCTTTC 1412
QY 461 TPPIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaIleHisAsp 480
DB 1413 TGGATCGAATTTGTATGATGGCCACAAAGAGGCCAAGCAGCTCGATCAGCTCCATGAC 1472
QY 481 LeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
DB 1473 CTCACCTGGTTCCACACACTCTATAGATGGATTGGGTTCTGTGCTGCTGTGGCA 1532
QY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
DB 1533 ACTGCTATATCTTGTGTACAAAAATGTTTTTATTTCTGTCAAAAATTTAATATAACT 1592
QY 521 ArgLysIleGluLysArgGlu 527
DB 1593 AGAAAGATTGAAAGAGGCA 1613

RESULT 6
US-09-981-353-83
; Sequence 83, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID NO. US20020160382A1 255002.4
; NAME/KEY: unsure
; LOCATION: 232, 243-244
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OTHER INFORMATION: Genbank Accession No. US20020142981A1 008834

US-09-880-107-3292

Alignment Scores:

Pred. No.:	5,96e-195	Length:	2090
Score:	1713.00	Matches:	327
Percent Similarity:	76.09%	Conservative:	74
Best Local Similarity:	62.05%	Mismatches:	114
Query Match:	61.13%	Indels:	12
DB:	10	Gaps:	5

US-09-784-340-2 (1-527) x US-09-880-107-3292 (1-2090)

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QY 9 ValPheLeuLeuLeuLeuLeuPheCys---ValGlyCysGlyPheCysGlyValLeu 27
    |||||
DB 43 GCTTTCTGCTGATACAGCTCAAGTTTACTTACTTACGCTGGAGCGTGGAAAGTGCTA 102
    |||||

QY 28 ValTTPProCysAspMetSerHisTTPLeuAsnValLysValLLeuLeuGluLeu 47
    |||||
DB 103 GCTGCCCCACAGAAATACGCCATTCGATTAATATAGAGCAATCCCGAAGAGCTTGTT 162
    |||||

QY 48 ValArgGlyHisGluValThrValLeuThrHisSerLysProSerLeuLeuAspTyrArg 67
    |||||
DB 163 CAGAGGGGATAGAGGTGCTGTTGACATCTTCGCTTACTCTTGTCATTCAGCCAGT 222
    |||||

QY 68 LysProSerAlaLeuLysPheGluValValHisMetProGlnAspArgThrGluIAsn 87
    |||||
DB 223 AATCATCTCGCATTAATAATTAGAAAGT-----TATCCTACATCTTAACATAAAATGAT 276
    |||||

QY 88 GluIlePheValAspLeuAlaLeuAsnValLeuPro-----GlyLeuSerThr 103
    |||||
DB 277 -----TTGGAAGATCTCTTCGAAAAATTCGATAGATGATATATGCTGTTCCAAA 330
    |||||

QY 104 -----TTPGlnSerValIleLysLeuAsnAspPhePheValIleuLeuGlyThr 120
    |||||
DB 331 AATACATTTTGGCATATTTTTCACAAATTCACAGAAATGTGTTGGAAATTAATGACTAC 390
    |||||

QY 121 LeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnIu 140
    |||||
DB 391 AGTAACAACCTCTGTAACATGATGCAATTTGTAATGAACCTTATGATGAACACACAGAG 450
    |||||

QY 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
    |||||
DB 451 TCAAAGTTTGATGTCATCTGCGCAGATGCCCTTAATCCCTGCTGAGCTACGCTGAGAA 510
    |||||

QY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysMetGluArg 180
    |||||
DB 511 CTAATTAACAATACCTTTCTGTACAGCTTCGATCTCTGTTGGTACACATTTGAGAG 570
    |||||

QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
    |||||
DB 571 AATGGGGAGAGATTTCTGTTCCCTCTCTATGATACCTGTTGTATGTCAGAAATTAAGT 630
    |||||

QY 201 AspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
    |||||
DB 631 GATCAAAATATTTTCTGAGAGAGATAAAAAATATGATACATATCTTATTTTGTACTTT 690
    |||||

QY 221 TTPIleGluAspTyrAspTyrHisPheTTPGluIuPheTyrSerLysAlaLeuGlyArg 240
    |||||
DB 691 TGGTTTCAAAATTTATGATGTGAAGAAATGGACACAGTTTATATAGTAAGCTTCAGAGAA 750
    |||||

QY 241 ProThrThrLeuCysGlnThrValGlyLysAlaGluIleTyrLeuIleArgThrTyrTrp 260
    |||||
DB 751 CCCACTACATTTATTTGAGACATGGGGAAGCTGAATGTGCTCATTTGCAACCTATTGG 810
    |||||

QY 261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyLeuHisCys 280
    |||||
DB 811 GATTTTGAATTTCTCGCCCATCTTCAACAAATGTTGATTTGTTGAGAGACTTCACTGT 870
    |||||

QY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyLysAsp 300
    |||||
DB 871 AAACCAAGCCAAACCCCTGCTTAAGAAATGAGAGAGCTTTGTTCAGAGCTCTGAGAGAAAT 930
    |||||

QY 301 GlyIleValAlaPheSerLeuGlySerLeuPheGlnAsnValThrGluIuLysAlaAsn 320
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DB 931 GGTATTTGGTGTCTCTGGGCTGATGATCAGTAACATGTCAAGAAAGTGGCAAC 990
    |||||

QY 321 IleIleIleSerAlaLeuAlaGluIleProGlnLysValLeuThrArgTyrLysGlyLys 340
    |||||
DB 991 ATGATTTGCATCAGCCCTTCCAGATCCACAAAGAGTTCATATGAGATTTGATGGCAAG 1050
    |||||

QY 341 LysProSerThrLeuGlyLysAsnThrArgLeuTyrAspTyrIleProGlnAsnAspLeu 360
    |||||
DB 1051 AAGCCAAATACATTTAGTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1110
    |||||

QY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlu 380
    |||||
DB 1111 CTGGTCATCCCAAAACCAAGCTTTTATACATGATGATGATGATGATGATGATGATGATGATGAT 1170
    |||||

QY 381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAsnAsp 400
    |||||
DB 1171 GCGATCTACCATGGGATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1230
    |||||

QY 401 IleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSer 420
    |||||
DB 1231 ATTGCTCATATGAAGCCAGAGGAGCGCCCTCAGTGTGACATCAGGACCATGTCAAAT 1290
    |||||

QY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
    |||||
DB 1291 AGAGATTTGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1350
    |||||

QY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
    |||||
DB 1351 ATGAATTTTCAGAAATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1410
    |||||

QY 461 TTPIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
    |||||
DB 1411 TGGATGAGTTTGTCTGTCGCGCACAAGAGGACCAACACCTTCGATGCTCCACTCACAAC 1470
    |||||

QY 481 LeuThrTTPPheGlnIleTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
    |||||
DB 1471 CTCACCTGGATGCAGTACACACCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1530
    |||||

QY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
    |||||
DB 1531 ACTGATGATTTATATCATCAAAATTTTCCGTTGTTGTTCCGAAAGCTTCCCAAAACA 1590
    |||||

QY 521 ArgLysIleGluLysArgGlu 527
    |||||
DB 1591 GGAAAGAGAGAAAGAGAT 1611
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RESULT 8
US-09-981-353-45
; Sequence 45, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 255115.4
; NAME/KEY: unsure
; LOCATION: 2087, 2089, 2094, 2096-2098, 2108, 2110, 2112, 2115-2116, 2120,
; LOCATION: 2122-2123, 2125, 2136
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-45
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Qy	280	CysLysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyGlu	299
Db	875	TGCAAACTCTCCAAACCCCTGGCTTAAGGAAATGGAAGACTTTTGACAGACTCTGGAGAA	934
Qy	300	AspGlyLLeValValPheSerLeuGlySerLeuPheGlnAsnValLTrnGluGluVal	319
Db	935	AATGCTGTGGGGTGGTTCCTGGGGTCAATAGCTCACTAACATGACAGAAAGAGGCC	994
Qy	320	AsnLLeuLeuAsnValAlaLeuAlaGlnLLeuProGlnLysValLeuTrpAlaGlyLysGly	339
Db	995	AACGTAATGTGATGACGCCCGCCGACGATCCCAAAAGAGTCTGTGGAGATTGATGAGG	1054
Qy	340	LysLysProSerThrLeuGluGlyAlaAsnTrpArgLeuTyrAspTrpLLeuProGlnAsnAsp	359
Db	1055	AATAAACCACTACTCTAGGTCTCAATCTACTCGGCTCTACAGTGGATPCCCCAATAGAC	1114
Qy	360	LeuLeuGlyHisProLysThrLysAlaPheLLeuThrHisGlyGlyMetAsnGlyLLeuTyr	379
Db	1115	CTTCTAGGTCTATCCAAAGACACAGCTTTTATACATCAGTGGAGGCCAATGGCATCTAC	1174
Qy	380	GluAlaLLeuTyrHisGlyValProMetValGlyValProLLeuPheGlyAspGluLeuAsp	399
Db	1175	GAGGCAATCTACCTAGGATGCCCTATGGTGGGATTCCTCTGTTCGTGATCAACCTGAT	1234
Qy	400	AsnLLeuAlaHisMetLysAlaLysGlyAlaAlaValAlaGluLLeuAsnPheLysThrMetThr	419
Db	1235	AACATTCGTCACTCAATGAAGGCCGAGGAGCAGCTGTAGAGTGAGACTTCAACACATGCG	1294
Qy	420	SerGluAspLeuLeuAlaValAlaLeuArgThrValLLeuThrAspSerSerTyrLysGluAsn	439
Db	1295	AGTACAGACTGGCTGTAATGATGCTTGTAAAGAGTAAATTAATGATTCCTCATATTAAGAGAT	1354
Qy	440	AlaMetArgLysSerArgLLeuHisHisAspGlnProValLysProLeuAspArgAlaVal	459
Db	1355	GTTATGAAATTTATCAAGAATTCACATGATGATCAACAGCAGTGAAGCCCTGTGATGACACTG	1414
Qy	460	PheTrpLLeuGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerLLeuAlaHis	479
Db	1415	TTCGTGATTGAAATTTGTCATCGGCACAAAGAGACTTAACACCTTGGGTTGCAGCCAC	1474
Qy	480	AspLeuThrTrpPheGlnHisTyrSerLLeuAspValLLeuGlyPheLeuLeuThrCysVal	499
Db	1475	GACCTACCTGGTTCCAGACACACACTTGGATGTGATGGGTTCCTGCTGCTGTGTG	1534
Qy	500	AlaThrAlaLLeuPheLeuPheThrLysCysPheLeuPheSerCysLLeuLysPheAsnLys	519
Db	1535	GCAACGTGATATTATATGCTCAAAATGTTGCTGTTTGTTCCTTGTGGAAGTTTGCTAGA	1594
Qy	520	ThrArgLysLLeuGluLysArgGlu	527
Db	1595	AAAGCAAAAGAGGAAAAAATGAT	1618
RESULT 13			
US-09-880-107-2120			
Sequence 2120, Application US/09880107			
Patent No. US20020142981A1			
GENERAL INFORMATION:			
APPLICANT: Horne, Darci T.			
APPLICANT: Vockley, Joseph G.			
APPLICANT: Scherf, Uwe			
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
FILE REFERENCE: 44921-5028-WO			
CURRENT APPLICATION NUMBER: US/09/880,107			
CURRENT FILING DATE: 2001-06-14			
PRIOR APPLICATION NUMBER: US 60/211,379			
PRIOR FILING DATE: 2000-06-14			
PRIOR APPLICATION NUMBER: US 60/237,054			
PRIOR FILING DATE: 2000-10-02			
NUMBER OF SEQ ID NOS: 3950			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2120			
LENGTH: 1855			

TYPE:	DNA	ORGANISM:	Homo sapiens
FEATURE:			
OTHER INFORMATION:	Genbank Accession No.	US20020142981A1	J05428
	US-09-880-107-2120		
Alignment Scores:			
Pred. No.:	1,15e-190	Length:	1855
Score:	1676.50	Matches:	320
Percent Similarity:	73.30%	Conservative:	67
Best local Similarity:	60.61%	Mismatches:	138
Query Match:	59.83%	Indels:	3
DB:	10	Gaps:	3
US-09-784-340-2 (1-527) x US-09-880-107-2120 (1-1855)			
QY	3	SeraplyssersralaleuValPheleuleuleuGlnleu---	PhecyValaGlyCysGly 21
DB	18	TCGTGAAATGAGACTTCAGTAAATTTCTATATACACTGACCTTTTGTACCTGGG	77
QY	22	PhecyGlyValleuValTrpCysaspMetSerHisTrpIleuAsnValVal	41
DB	78	AATGTGGAAGGCGTGTGGTGGCAGCAGAAATACAGCCATTGAGATATTAAGACA	137
QY	42	IleuGlnGluIleuValIleValGlyHisGluValThrValIleuThrHisSerLysPro	61
DB	138	ATTCCTGATGAGCTTATTCAGAGAGGCTCATGAGCTGACTGACCTTCAGCTTCC	197
QY	62	SerleuIleaspyrTrpArgLysProSerAlaIleuLysPheGluValValHisMetProGln	81
DB	198	ATTCCTTTTGTATCCCAACACTCATCCGCTTTTAAATTAATTAATTTCCACATCTTTA	257
QY	82	AspArgThrGlu--GluAsnGluIlePheValaspleu--AlaIleuAsnValleuPro	99
DB	258	ACTAAACTGAGTGGAGAAATTCATCATGCAACAGATTAAAGATGCTGACACTTCCA	317
QY	100	GlyLeuSerThrTrpGlnSerValIleIleLysLeuAsnAspPhePheValGluIleArgGly	119
DB	318	AAAGATACATTTGCTTATATTTTTCACAAGTACAGCAAAATCATGTCATATTTGGTAC	377
QY	120	ThrleuLysMetMetCysGlnSerPheIleIleTrpAsnGlnIleuMetLysLysLeuGln	139
DB	378	ATAACTGAAAGCTTCGTAAGAGATGATGTTCAATTAAGAAATTTAAGAAAAAGTACAA	437
QY	140	GluThrAsnTrpAspValMetLeuIleAspProValIleProCysGlyAspAspMetAla	159
DB	438	GAGTCACAGATTGACGTCATTTTGGCAGATGCTATTTTCCCTGATGAGCTGCTGGCT	487
QY	160	GluLeuLeuAlaValProPheValLeuThrIleuArgIleSerValGlyGlyAsnMetGlu	179
DB	498	GAGCATATTACATACACCTTTGTGTACAGTCTCAGCTTCCTCTCTGCTACACTTTTGA	557
QY	180	ArgSerCysGlyLysLeuProAlaProLeuSerTrpAlaProValProMetThrGlyLeu	199
DB	558	AAGCATAGTGAAGGATTTATTTTCCCTCTTCCTACCTACCTGCTTTTATGTGCAATT	617
QY	200	ThrAspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerValleuPheHis	219
DB	618	ACTGATCAAAAGACTTTCATGAGAGAGGTTAAAAATATGATCTATGTGCTTACTTTGAC	677
QY	220	PheTrpIleGlnAspTrpAspTrpHisPheTrpGlnIleuPheTrpSerLysAlaLeuGly	239
DB	678	TTTTTGTCGCAAAATATTGTCATGAAAGAGGGATGAGTTTATATGAAAGTTTCAGGA	737
QY	240	ArgTrpThrThrIleuCysGluThrValGlyLysAlaIleuIleTrpIleuIleArgThrTrp	259
DB	738	AGACCCACTACGTTATCTGACACATGAGGGAACCTCAGTATGCGCTTATTCGAAACTCC	797
QY	260	TrpAspPheGluPheProGlnProTrpGlnProAsnPheGluPheValGlyGlyLeuHis	279
DB	798	TGGAATTTTTCGTTCTCTCATACCCACGCTTACCAAAATGTGATTTTGTGGAGACATCCAC	857
QY	280	CysLysProAlaLysAlaLeuProLysGluMetClnAsnPheValGlnSerSerGlyLys	299

Db	858	TGCAAACTGCGCAAAACCCCTGGCTTAAGAAATGCAAGACTTTGTACAGAGCTTCGAGAA	917
Qy	300	AspAllyleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluLysAla	319
Db	918	AATGGTGTGTGGTGTCTTCTCTGGGGTCAATGTGTACATGACATGCAGAAAGAGGCC	977
Qy	320	AsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuThrPArgTyrLysGly	339
Db	978	AACGTAAATGCATAGCGCCGCGCCAGATGCCCAAAAGAGTTCTGGAGATTGATGG	1037
Qy	340	LysLysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrpIleProGlnAsnAsp	359
Db	1038	AATAAACCAAGTACTCTTACGTGTCTCAATACTCGGCTGTAAATAGTGATACCCAGAAATAC	1097
Qy	360	LeuLeuGlyHisProLysThrLysIleAlaPheIleThrHisGlyGluMetAsnGlyLeuTyr	379
Db	1098	CTTCTAGGTATCCAAAGACCAAGACGTTTATTAACATCATGTGGAGACCATGGCATCTAC	1157
Qy	380	GluAlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAsp	399
Db	1158	GAGGCATCTACCATGGGATCCCTATGGTGGGATTCATGTCTGTTGGCGATCAACCTGAT	1217
Qy	400	AsnIleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPhelYsThrMetThr	419
Db	1218	AACATTCCTCACATGAAGCCACGAGGACGACGCTGTACAGTGCATCAACACATGTGCG	1277
Qy	420	SerLysLysLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsn	439
Db	1278	AGTACAGACTGTGGAAATGGATGGATTGAAGAGAGTAAATTAATGATCTTCATATTAACAGAT	1337
Qy	440	AlaMetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAsnParGluAla	459
Db	1338	GTTATGAATTAATCAAGAATTAACAACTGATCAACAGCATGAACCCCTGGATGAGACATC	1397
Qy	460	PheTrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaHis	479
Db	1398	TTCTGAGTTAAATTGTCATGCATGCCCCCAAAAGAGCTAAACACCTTCGGGTTGCACCCAC	1457
Qy	480	AspLeuThrTrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysVal	499
Db	1458	GACCTCACCTGGTTCAGATCCACTCTTTGGAGTGTATGGGTCTCTGCTGCTGTGTG	1517
Qy	500	AlaThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLys	519
Db	1518	GCACTGTGATATTATCGTCGCAAAATGTGTGTCTGTTTCTGCGAAGTTGCTAGA	1577
Qy	520	ThrArgLysIleGluLysArgGlu	527
Db	1578	AAAGCAAAAGAGGAAAMAATGAT	1601
RESULT 14			
US-09-880-107-3756 Application US/09880107			
Patent No. US20020142981A1			
GENERAL INFORMATION:			
APPLICANT: Horne, Darci T.			
APPLICANT: Vockley, Joseph G.			
APPLICANT: Schert, Uwe			
APPLICANT: Gene Logic, Inc.			
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
FILE REFERENCE: 44921-5028-WO			
CURRENT APPLICATION NUMBER: US/09/880,107			
CURRENT FILING DATE: 2001-06-14			
PRIOR APPLICATION NUMBER: US 60/211,379			
PRIOR FILING DATE: 2000-06-14			
PRIOR APPLICATION NUMBER: US 60/237,054			
PRIOR FILING DATE: 2000-10-02			
NUMBER OF SEQ. ID NOS: 3950			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 3756			
SEQ ID NO 3756			
LENGTH: 2799			
TYPE: DNA			

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